

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 30, 2005, 19:33:36 ; Search time 176 Seconds
(without alignments)

480.074 Million cell updates/sec

Title: US-09-786-867C-5

Perfect score: 893

Sequence: 1 MTTASTSQVRQNYHQDSEAA.....PRRRKRPHSIPTILIFRSP 165

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	890	99.7	165	2 Q8TD27	Q8td27 homo sapien
2	615.5	68.9	232	2 Q6NS36	Q6ns36 homo sapien
3	610.5	68.4	182	1 FR1H HUMAN	P02794 homo sapien
4	605.5	67.8	183	2 Q6NZ44	Q6nz44 homo sapien
5	589.5	66.0	182	1 FR1H TRIVU	Q9xt73 trichosurus
6	589.5	66.0	183	2 Q9SMP7	Q9sm73 canis faml
7	586.5	65.7	182	2 Q920K4	Q920k4 cavia porce
8	585	65.5	197	2 Q6P9V2	Q6p9v2 rattus norv
9	583.5	65.3	220	2 Q6GH15	Q6gh15 rattus norv
10	583.5	65.3	229	2 Q6AYV6	Q6ayv6 rattus norv
11	580.5	65.0	185	1 FR1H CRIGR	P29389 cricetus
12	575.5	64.4	181	1 FR1H MOUSE	P09528 mus musculus
13	573.5	64.2	181	1 FR1H RAT	P19132 rattus norv
14	570.5	63.9	182	2 Q8M1P0	Q8m1p0 equus cabal
15	560.5	62.8	170	1 FR1H SHEEP	P16685 ovis aries
16	560.5	62.8	179	1 FR1H CHICK	P08267 gallus gall
17	560.5	62.8	180	1 FR1H BOVIN	Q46414 bos taurus
18	560.5	62.8	181	2 Q6PRV1	Q6prv1 coturnix co
19	516.5	57.8	177	2 Q7ZXM8	Q7zxm8 xenopus lae
20	515.5	57.7	177	2 Q6DDB5	Q6ddb5 xenopus tro
21	514.5	57.6	169	2 Q8HZP4	Q8hzp4 bos taurus
22	514.5	57.6	177	1 FR1H XENLA	Q78xa6 xenopus lae
23	508.5	56.9	180	1 FR1H PIG	P19130 sus scrofa
24	500	56.0	157	2 Q7ZZT8	Q7zzt8 oreochromis
25	499.5	55.9	164	1 FR1H RABIT	P25915 oryctolagus
26	494	55.3	100	2 Q8G2J4	Q8g2j4 bos taurus
27	494	55.3	242	2 Q8NAE7	Q8nae7 homo sapien
28	488.5	54.7	152	2 Q6EBB2	Q6eb2 latimeria c
29	480	53.8	132	2 Q6Y241	Q6y241 pagrus major
30	479	53.6	237	2 Q9D5F4	Q9d5f4 mus musculus
31	477	53.4	262	2 Q9D5H4	Q9d5h4 mus musculus

32 475 53.2 177 1 FR1H SALSA P49946 salmo salar
33 469 52.5 177 2 Q9DDT0 Q9ddt0 brachydanio
34 460.5 51.6 175 2 Q801J6 Q801j6 scyliorhinu
35 458 51.3 177 2 Q66HX7 Q66hx7 brachydanio
36 457 51.2 92 2 Q862D5 Q862d5 bos taurus
37 456.5 51.1 127 2 Q862R4 Q862r4 bos taurus
38 453 50.7 176 2 Q98TT0 Q98tto oncorhynchus
39 441 49.4 156 2 Q6EBB1 Q6eeb1 protopteris
40 440 49.3 177 2 Q801J5 Q801j5 petromyzon
41 439 49.2 173 1 FR1S LYMST P42577 lymanaea sta
42 436 48.8 134 2 Q86QN8 Q86qn8 branchiostoma
43 436 48.8 172 2 Q6WNW7 Q6wnw7 branchiostoma
44 435.5 48.8 149 2 Q9GMG9 Q9gm9 macaca mulatta
45 435.5 48.8 174 2 Q86LZ3 Q86lz3 branchiostoma

ALIGNMENTS

RESULT 1
Q8TD27 PRELIMINARY; PRT; 165 AA.
AC Q8TD27; Q8TD27; 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Placenta immunoregulatory factor PLIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21935397; PubMed=11821435; DOI=10.1074/jbc.M200956200;
RA MOROZ C., Traub L., Maymon R., Zahalka M.A.;
RT "PLIF, a novel human ferritin subunit from placenta with
immunorepressive activity."
RL J. Biol. Chem. 277:12901-12905 (2002).
CC -|- SIMILARITY: Belongs to the ferritin family.
CC -|- SIMILARITY: Contains 1 ferritin-like diiron domain.
DR EMBL; AY033611; AAK55486.1; -
DR HSRF; P02794; 2FHA.
DR GO; GO:0005886; C:plasma membrane; NAS.
DR GO; GO:0019900; F:kinase binding; NAS.
DR GO; GO:0006955; P:immune response; IDA.
DR GO; GO:0008285; P:negative regulation of cell proliferation; IDA.
DR InterPro; IPR001519; Ferritin.
DR InterPro; IPR009078; Ferritin/RR_like.
DR InterPro; IPR008331; Ferritin Dps.
DR InterPro; IPR009040; Ferritin_like.
DR Pfam; PF00210; Ferritin; 1.
DR ProDom; PD000971; Ferritin; 1.
DR PROSITE; PS00540; FERRITIN_1; 1.
DR PROSITE; PS0905; FERRITIN_LIKE; 1.
DR Iron; Iron storage; Metal-binding.
SQ SEQUENCE 165 AA; 19490 MW; C4849C85FCABAB6 CRC64;

Query Match 99.7%; Score 890; DB 2; Length 165;
Best Local Similarity 99.4%; Pred. No. 1.1e-71;
Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHQSS 60
DB 1 MTTASTSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYFDRDDVALKNFAKYLHQSS 60
QY 61 HEERQHAELKMLQNRQGRIFLODIKPPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120
DB 61 HEERQHAELKMLQNRQGRIFLODIKPPDCDDWESGLNAMECALHLEKNVNSLLEPPS 120
QY 121 PISPSPCWHYTTNRPOQHLLRPRRRKRPHSIPTILIFRSP 165
DB 121 PISPSPCWHYTTNRPOQHLLRPRRRKRPHSIPTILIFRSP 165